

- 1 -

piece 1, NC_000913, plsB_dgkA+, config: linear, direction: +, begin: 4254460, end: 4254679

This diagram illustrates the protein sequence alignment for *NQ_000013_nleB*. The top row shows the DNA sequence with codon positions (e.g., *4254460, *4254470, *4254480, *4254490, *4254500, *4254510, *4254520, *4254530, *4254540) and corresponding amino acids. Red dots indicate stop codons. The bottom row shows the resulting protein sequence: phe-val-val-asn-ser-trp-pro-alal-gly-his-lys-arg-cys-lys-alal-ser-gly-leu-cys-ser-lys-phe-val-alaser-arg-thr-fMet. A green box highlights a domain spanning positions 4254510 to 4254530, which includes the sequence alatgcaaaatgcggcaggatagca. Below the sequence, a dashed line indicates the secondary structure of the protein, featuring various loops and connections between residues.

.....] NC_000913.pisB

நெடுஞ்செழிய மாநகரம்

----- ... sd-(14)-ir 4254548 Gap

----- ... sd-ir 4254548 plsB_dgkA+

5' g a a a g t c a t g g g a a a t t c t g t g g t a t c c g c t c a t g t t t c g g c g g c g c t a c g c a a a a c c c g a a t c a t c g g a t t a a c g g t a c 3'

- - fMet - gly - asn - ser - val - val - ser - ala - his - val - ser - arg - gly - ala - thr - gln - thr - arg - ile - ile - gly - phe - asn - gly - thr -

- lys - ser - trp - glu - ile - leu - trp - tyr - pro - leu - met - phe - arg - ala - ala - leu - arg - lys - pro - glu - ser - ser - asp - leu - thr - val - his

plsB dgkA+

p35 4.1 bits

```
... ----- } sd-(14)-ir 4254548 Gap 4.9 bits  
... ----- sd-ir 4254548 plsB_dgKA+ total 6.4 bits
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----- ... p35-(26)-p10 4254638 Gap
p35-p10 4254638 total 5

----- ... p35-p10 4254638 total 5.

5' * *4254630 * *4254640 * *4254650 *

act gat att gag cta atg taaaagg ttct

- -

leu - ile - leu - thr - leu - ile - met -

... [###] orf 33 codons

p35-(26)-p10 4254638 Gap 3.7 bits

The diagram illustrates the gene structure of *plsB_dgkA+*. The top part shows the DNA sequence with transcription start sites at positions 115900 and 125107, indicated by arrows pointing upwards. The bottom part shows the mRNA transcript with the amino acid sequence: fMet - ala - asn - ser - thr - thr -. The gene is annotated as *plsB_dgkA+* and is associated with the NC_000913.dgk genome.

प्राचीनता p10 4.6 bits

... -----| p35-p10 4254638 total 5.9 bits

|-----| sd-ir 4254660 plsB_dgkA+ total 11.9 bits

Digit p35 3-4 bits

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{-----} p35-(24)-p10 4254667 Gap 2.4 bits
{-----} p35-p10 4254667 total 5.6 bits